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Range: from ⎡begin⎤ to ⎡end⎤   ☐ Reverse complemented strand   Features: ☐SNP ☐CDD
☑MGC

☐1: XM_211174. Reports PREDICTED: Homo s...[gi:27483466]   Links

```
LOCUS       XM_211174               1021 bp    mRNA    linear   PRI 20-AUG-2004
DEFINITION  PREDICTED: Homo sapiens hypothetical LOC283710 (LOC283710), mRNA.
ACCESSION   XM_211174
VERSION     XM_211174.1  GI:27483466
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
COMMENT     MODEL REFSEQ:  This record is predicted by automated computational
            analysis. This record is derived from an annotated genomic sequence
            (NT_010194) using gene prediction method: GNOMON, supported by EST
            evidence.
            Also see:
                Documentation of NCBI's Annotation Process

FEATURES             Location/Qualifiers
     source          1..1021
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="15"
     gene            1..1021
                     /gene="LOC283710"
                     /note="Derived by automated computational analysis using
                     gene prediction method: GNOMON."
                     /db_xref="GeneID:283710"
                     /db_xref="InterimID:283710"
     CDS             106..510
                     /gene="LOC283710"
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                     /protein_id="XP_211174.1"
                     /db_xref="GI:27483467"
                     /db_xref="GeneID:283710"
                     /db_xref="InterimID:283710"
                     /translation="MGVFTMQGQGIPCCSTIRFGTPPPPRPHQRASAMPRRGPQQTRQ
                     DPPVGPKAGGRAAPPNSQDACSTPHAPLSASGEHPATPRHTHPGYIPPSHAWSGALEM
                     SEIQAFPKESGLEGGLPPFAELHMTTADDRPH"
ORIGIN
        1 aaggatgagc aggctctctg ccatctgccc accaactttt caagttactt ttacccacct
       61 tcaaaattac atctgctttt agcaagaatt actgatgtga taaagatggg agtgttcacc
      121 atgcaagggc aggggatccc ctgctgctcc accatcagat ttgggacacc accccccccc
      181 cggccccacc agagggcatc agctatgcct agaaggggac cacaacagac tcgacaggat
      241 ccaccggttg ggcccaaggc aggaggaagg gcggcgcccc caaactccca ggacgcctgc
      301 agcacccccc acgcgccgct ctccgcctct ggggagcatc ctgccacccc ccgacacaca
      361 caccccggct acatcccgcc ttctcacgct tggtcaggcg ctctggagat gtcggagatc
      421 caggcttttc ctaaagagtc aggattggaa ggcggactcc caccgtttgc tgagctccac
      481 atgacaacag cagacgacag gccgcactga tcccacctgg cttacaggtg ctgtcacaca
```

```
541 ggtacgcctt cttgtgaatc atcagtcacc atttgcccct cgcagcaacc ctgtcttgga
601 ggaaggtcct tgccgacacc cgcctctccc cacccttagg ctcccttgct ccttcattca
661 accattgttt acatgtcgtt caggactgct gactaaacac tttcaagcac agtggaccct
721 tgaacaacgc aggttcaaac tgtgcaggtc cacccacagg gatgtttttc aatcagagtt
781 ataccaagtg tccctgcctc tcctgcctcc cttcccactt cctccatgtc ttcctctctg
841 ccaccctgag gcagcaagac cagcccctcc tcctcagcca ctcaacatga agacaacgag
901 gatgaagact tctatgataa tccacttcca cttagtaaat gctttctctt atgatattct
961 taatgacatt ttattttccc aagcttagtt tattgtaaga atacagtata aatacacata
1021 c
//
```

Dec 16 2004 18:01:17

Sequence Revision History

PubMed | Nucleotide | Protein | Genome | Structure | PMC | Taxonomy | OMIM | Books

Find *(Accessions, GI numbers or Fasta style Seqlds)* XM_211174

About Entrez

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│ Show difference in BLAST   format Show │
└─────────────────────────────┘

Entrez

Gi	Version	Update Date
27483466	1	Aug 20 2004 9:44 AM
27483466	1	Apr 28 2003 1:46 PM

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LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

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LocusLink

```
Query= gi|27483466|ref|XM_211174.1| PREDICTED: Homo sapiens
hypothetical LOC283710 (LOC283710), mRNA
         (1021 letters)

<gi|27483466|ref|XM_211174.1| Homo sapiens LOC283710 (LOC283710), mRNA
         Length = 1021

 Score = 1965 bits (991), Expect = 0.0
 Identities = 1011/1021 (99%)
 Strand = Plus / Plus

Query: 1    aaggatgagcaggctctctgccatctgccaccacttttcaagttacttttacccacct  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    aaggatgagcaggctctctgccatctgccaccacttttcaagttacttttacccacct  60

Query: 61   tcaaaattacatctgctttagcaagaattactgatgtgataaagatgggagtgttcacc  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   tcaaaattacatctgctttagcaagaattactgatgtgataaagatgggagtgttcacc  120

Query: 121  atgcaagggcaggggatcccctgctgctccaccatcagatttgggacaccannnnnnnnn  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  atgcaagggcaggggatcccctgctgctccaccatcagatttgggacaccaccccccccc  180

Query: 181  nggcccaccagagggcatcagctatgcctagaagggggaccacaacagactcgacaggat  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  cggccccaccagagggcatcagctatgcctagaagggggaccacaacagactcgacaggat  240
```

Clusters of orthologous groups

Protein reviews on the web

```
Query: 241  ccaccggttgggcccaaggcaggaggaggggcggcgccccaaactcccaggacgccctgc  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  ccaccggttgggcccaaggcaggaggaggggcggcgccccaaactcccaggacgccctgc  300

Query: 301  agcacccccacgcgccgctctccgcctctgggggagcatcctgccaccccgacacaca  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  agcacccccacgcgccgctctccgcctctgggggagcatcctgccacccccgacacaca  360

Query: 361  caccccggctacatccgcctctcacgcttggtcaggcgctctggagatgtcggagatc  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361  caccccggctacatccgcctctcacgcttggtcaggcgctctggagatgtcggagatc  420

Query: 421  caggctttcctaaagagtcaggattggaaggcggactcccacgtttgctgagctccac  480
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Sbjct: 421  caggctttcctaaagagtcaggattggaaggcggactcccacgtttgctgagctccac  480

Query: 481  atgacaacagcagacagccgcactgatcccacctgcttacaggtgctgtcacaca  540
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  atgacaacagcagacagccgcactgatcccacctgcttacaggtgctgtcacaca  540

Query: 541  ggtacgccttcttgtgaatcatcagtcaccatttgccctcgcagcaaccctgtcttgga  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query: 601  ggaaggtccttgccgacaccccgcctctcccacccttaggctccctttgctccttcattca  660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601  ggaaggtccttgccgacaccccgcctctcccacccttaggctccctttgctccttcattca  660

Query: 661  accattgttacatgtcgttcaggactgctgactaaacactttcaagcacagtggaccct  720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```

```
Query: 721  tgaacaacgcaggttcaaaactgtgcaggtccaccacaggggatgtttttcaatcagagtt  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721  tgaacaacgcaggttcaaaactgtgcaggtccaccacaggggatgtttttcaatcagagtt  780

Query: 781  ataccaagtgtccctgcctcctgcctccctcccacttcctcctccatgtcttcctctctg  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781  ataccaagtgtccctgcctcctgcctccctcccacttcctcctccatgtcttcctctctg  840

Query: 841  ccaccctgaggcagcaagaccagccctcctcctcagccactcaacatgaagacaacgag  900
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Sbjct: 841  ccaccctgaggcagcaagaccagccctcctcctcagccactcaacatgaagacaacgag  900

Query: 901  gatgaagacttctatgataatccacttccacttagtaaatgctttctcttatgatattct  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901  gatgaagacttctatgataatccacttccacttagtaaatgctttctcttatgatattct  960

Query: 961  taatgacatttattttcccaagcttagtttattgtaagaatacagtatataaatacacata  1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 961  taatgacatttattttcccaagcttagtttattgtaagaatacagtatataaatacacata  1020

Query: 1021 c  1021
            |
Sbjct: 1021 c  1021


Score = 32.2 bits (16), Expect = 2e-04
Identities = 16/16 (100%)
Strand = Plus / Minus

Query: 129  gcaggggatcccctgc  144
            ||||||||||||||||
Sbjct: 144  gcaggggatcccctgc  129


Lambda     K      H
```

```
          1.37    0.711    1.31

Gapped
Lambda      K        H
          1.37    0.711    1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 3
Number of Sequences: 0
Number of extensions: 3
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 3
length of query: 1021
length of database: 1021
effective HSP length: 9
effective length of query: 1012
effective length of database: 1012
effective search space:  1024144
effective search space used:  1024144
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 9 (18.3 bits)
```

Sequence Revision History

PubMed | Nucleotide | Protein | Genome | Structure | PMC | Taxonomy | OMIM | Books

Find (*Accessions, GI numbers or Fasta style SeqIds*) XM_211174

About Entrez

Show difference in GenBank/GenPept Diff format [Show]

Entrez

Gi	Version	Update Date
27483466	1	Aug 20 2004 9:44 AM
27483466	1	Apr 28 2003 1:46 PM

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

```
Accession = XM_211174, Locus = XM_211174
==============================================

Differences in LOCUS names:
--------------------------
old:  "LOCUS      XM_211174          1021 bp   mRNA    linear   PRI
       28-APR-2003"
                 ^
new:  "LOCUS      XM_211174          1021 bp   mRNA    linear   PRI
       20-AUG-2004"
                 ^

Differences in DEFINITION:
--------------------------
old:  "Homo sapiens LOC283710 (LOC283710), mRNA."

new:  "PREDICTED: Homo sapiens hypothetical LOC283710 (LOC283710), mRNA."
                 ^

Differences in REFERENCE:
-------------------------
Old reference:
       refline:   "1  (bases 1 to 1021)"
       authors:   "International Human Genome Sequencing Consortium."
       title:     "The DNA sequence of Homo sapiens"
       journal:   "Unpublished (2003)"

Differences in COMMENT:
-----------------------
old:  "MODEL REFSEQ:  This record is predicted by automated computational
```

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Protein reviews on the web

analysis. This record is derived from an annotated genomic sequence
(NT_010194) using gene prediction method: BLAST, supported by EST
evidence. Also see: Documentation of NCBI's Annotation Process "

new: "MODEL REFSEQ: This record is predicted by automated computational
analysis. This record is derived from an annotated genomic sequence
(NT_010194) using gene prediction method: GNOMON, supported by EST
evidence. Also see: Documentation of NCBI's Annotation Process "

Differences in FEATURE.CDS:

Changed feature CDS   106..510
        New   /db_xref   = "GeneID:283710"

Differences in FEATURE.gene:

Changed feature gene   1..1021
        New   /db_xref   = "GeneID:283710"
        New   /note   = "Derived by automated computational
                                 analysis using gene prediction method:
                                 GNOMON."